Figure 1: Shows an alignment between SEQ ID NO:9 translated sequence (SEQ ID NO:11) with *pha*A.

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Seq ID 9 B-ketothiolase Re    (1)  MTREVVMVSGVRTAIGTFGGSLKDVAPAELGAEVVREALARAQVSGDDVG
              Our phaA        (1)  -VTEVVIVSAARTAVGKFGGSLAKIPAPELGAVVIKAALERAGVKPEQVS
              Consensus       (1)     DVVIVSA RTAIG FGGSL  I   ELGALVIK AL RA V   D V
                                   51                                              100
Seq ID 9 B-ketothiolase Re   (51)  HVMFGNVIQTEPRDMYLGRVAAMNGGVTINAPAITVNRICGSGLQAIMSA
              Our phaA       (50)  EVEMGSVITAGS-GQNPTRQAAIKAGIPAMVPAMTINKVCGSGLKAMMLA
              Consensus      (51)  VI GNVI         AR AAI AGL    PALTINKLCGSGL AIM A
                                   101                                             150
Seq ID 9 B-ketothiolase Re  (101)  ASTIILGDTDVAICGGAESMSRAPMIAPMYRWGARMGDAGLVDMMIG-ML
              Our phaA       (99)  ANAIMAGDAEIVMVAGGQENMSAAPHVLPGSRDGFRMGDAKLVDTMIVDGL
              Consensus     (101)  AN IL GD DI IAGG E MS APHL PAAR G RMGDA LVD MI  AL
                                   151                                             200
Seq ID 9 B-ketothiolase Re  (150)  HDPMHRIHMGVTAENVAKEYDISRAQQDEAALESHRRASAAIKAGYFKDQ
              Our phaA      (149)  WDVMNQYHMGITAENVAKEYGISREAQDEFAVGSQNKAEAAQKAGKFDEE
              Consensus     (151)   D F  HMGITAENVAKEY ISR QDE AL S  KA AA KAG F D
                                   201                                             250
Seq ID 9 B-ketothiolase Re  (200)  IVPVMSKGRK-GDVTFDTDEHVRHDATIDDMIKLRPVFVKENGTVTAGNA
              Our phaA      (199)  IVPVIIPQRKGDPVAFKTDEFVRQGATIDSMSGLKPAFDK-AGTVTAANA
              Consensus     (201)  IVPVL   RK   V F TDE VR  ATID MS LKP F K  GTVTAANA
                                   251                                             300
Seq ID 9 B-ketothiolase Re  (249)  SGLNDAAAAVVMMERAEAERRGLKPLAREVSYGHAGVDPKAMGIGPVPAI
              Our phaA      (248)  SGLNDGAAAVVMMSAAKAKELGLTPLATIKSYANAGVDPKVMGMGPVPAS
              Consensus     (251)  SGLNDAAAAVVMM  A A   GL PLA I SYA AGVDPK MGIGPVPAS
                                   301                                             350
Seq ID 9 B-ketothiolase Re  (299)  KIALERAGLQVSDLDVIEANEAFAAQACAVTKAIGLDPIKVNPNGSGISI
              Our phaA      (298)  KRALSRAEWTPQDLDLMEINEAFAAQALAVHQQMGWDTSKVNVNGGAIAI
              Consensus     (301)  K AL RA    DLDLIE NEAFAAQA AV   LG D AKVN NG AIAI
                                   351                                     397
Seq ID 9 B-ketothiolase Re  (349)  GHPIGAIGALITVKALHEINRVQGRYALVIMCIAIIFERI-------
              Our phaA      (348)  GHPIGASGCRILVTLLHEMKRRDAKKGLASICIGGMGVALAVERK-
              Consensus     (351)  GHPIGASG I V  LHEL R  AK AL SLCIAA
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